

PCT10

## RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/10/009,332

TIME: 12:00:35

Input Set : A:\Q67541 Sequence Listing.txt

Output Set: N:\CRF3\01142002\J009332.raw

**ENTERED**

3 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
 4 Kazusa DNA Research Institute  
 6 <120> TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING AGGREGANASE ACTIVITY  
 8 <130> FILE REFERENCE: Q67541  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/009,332  
 C--> 10 <141> CURRENT FILING DATE: 2001-12-10  
 10 <150> PRIOR APPLICATION NUMBER: JPA Hei 11-321740  
 11 <151> PRIOR FILING DATE: 1999-11-11  
 13 <150> PRIOR APPLICATION NUMBER: JPA 2000-144020  
 14 <151> PRIOR FILING DATE: 2000-05-16  
 16 <160> NUMBER OF SEQ ID NOS: 35  
 18 <170> SOFTWARE: PatentIn version 3.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 950  
 22 <212> TYPE: PRT  
 23 <213> ORGANISM: Homo sapiens  
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 28 1 5 10 15  
 31 Gly Gly Phe Glu Pro Glu Arg Glu Val Val Val Pro Ile Arg Leu Asp  
 32 20 25 30  
 35 Pro Asp Ile Asn Gly Arg Arg Tyr Trp Arg Gly Pro Glu Asp Ser  
 36 35 40 45  
 39 Gly Asp Gln Gly Leu Ile Phe Gln Ile Thr Ala Phe Gln Glu Asp Phe  
 40 50 55 60  
 43 Tyr Leu His Leu Thr Pro Asp Ala Gln Phe Leu Ala Pro Ala Phe Ser  
 44 65 70 75 80  
 47 Thr Glu His Leu Gly Val Pro Leu Gln Gly Leu Thr Gly Gly Ser Ser  
 48 85 90 95  
 51 Asp Leu Arg Arg Cys Phe Tyr Ser Gly Asp Val Asn Ala Glu Pro Asp  
 52 100 105 110  
 55 Ser Phe Ala Ala Val Ser Leu Cys Gly Gly Leu Arg Gly Ala Phe Gly  
 56 115 120 125  
 59 Tyr Arg Gly Ala Glu Tyr Val Ile Ser Pro Leu Pro Asn Ala Ser Ala  
 60 130 135 140  
 63 Pro Ala Ala Gln Arg Asn Ser Gln Gly Ala His Leu Leu Gln Arg Arg  
 64 145 150 155 160  
 67 Gly Val Pro Gly Gly Pro Ser Gly Asp Pro Thr Ser Arg Cys Gly Val  
 68 165 170 175  
 71 Ala Ser Gly Trp Asn Pro Ala Ile Leu Arg Ala Leu Asp Pro Tyr Lys  
 72 180 185 190  
 75 Pro Arg Arg Ala Gly Phe Gly Glu Ser Arg Ser Arg Arg Arg Ser Gly  
 76 195 200 205  
 79 Arg Ala Lys Arg Phe Val Ser Ile Pro Arg Tyr Val Glu Thr Leu Val  
 80 210 215 220  
 83 Val Ala Asp Glu Ser Met Val Lys Phe His Gly Ala Asp Leu Glu His  
 84 225 230 235 240

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87 Tyr Leu Leu Thr Leu Leu Ala Thr Ala Ala Arg Leu Tyr Arg His Pro
88                245                250                255
91 Ser Ile Leu Asn Pro Ile Asn Ile Val Val Val Lys Val Leu Leu Leu
92                260                265                270
95 Arg Asp Arg Asp Ser Gly Pro Lys Val Thr Gly Asn Ala Ala Leu Thr
96                275                280                285
99 Leu Arg Asn Phe Cys Ala Trp Gln Lys Lys Leu Asn Lys Val Ser Asp
100               290                295                300
103 Lys His Pro Glu Tyr Trp Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp
104 305                310                315                320
107 Leu Cys Gly Ala Thr Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly
108                325                330                335
111 Thr Met Cys Asp Pro Lys Arg Ser Cys Ser Val Ile Glu Asp Asp Gly
112                340                345                350
115 Leu Pro Ser Ala Phe Thr Thr Ala His Glu Leu Gly His Val Phe Asn
116                355                360                365
119 Met Pro His Asp Asn Val Lys Val Cys Glu Glu Val Phe Gly Lys Leu
120                370                375                380
123 Arg Ala Asn His Met Met Ser Pro Thr Leu Ile Gln Ile Asp Arg Ala
124 385                390                395                400
127 Asn Pro Trp Ser Ala Cys Ser Ala Ala Ile Ile Thr Asp Phe Leu Asp
128                405                410                415
131 Ser Gly His Gly Asp Cys Leu Leu Asp Gln Pro Ser Lys Pro Ile Ser
132                420                425                430
135 Leu Pro Glu Asp Leu Pro Gly Ala Ser Tyr Thr Leu Ser Gln Gln Cys
136                435                440                445
139 Glu Leu Ala Phe Gly Val Gly Ser Lys Pro Cys Pro Tyr Met Gln Tyr
140                450                455                460
143 Cys Thr Lys Leu Trp Cys Thr Gly Lys Ala Lys Gly Gln Met Val Cys
144 465                470                475                480
147 Gln Thr Arg His Phe Pro Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly
148                485                490                495
151 Lys Leu Cys Leu Lys Gly Ala Cys Val Glu Arg His Asn Leu Asn Lys
152                500                505                510
155 His Arg Val Asp Gly Ser Trp Ala Lys Trp Asp Pro Tyr Gly Pro Cys
156                515                520                525
159 Ser Arg Thr Cys Gly Gly Gly Val Gln Leu Ala Arg Arg Gln Cys Thr
160                530                535                540
163 Asn Pro Thr Pro Ala Asn Gly Gly Lys Tyr Cys Glu Gly Val Arg Val
164 545                550                555                560
167 Lys Tyr Arg Ser Cys Asn Leu Glu Pro Cys Pro Ser Ser Ala Ser Gly
168                565                570                575
171 Lys Ser Phe Arg Glu Glu Gln Cys Glu Ala Phe Asn Gly Tyr Asn His
172                580                585                590
175 Ser Thr Asn Arg Leu Thr Leu Ala Val Ala Trp Val Pro Lys Tyr Ser
176                595                600                605
179 Gly Val Ser Pro Arg Asp Lys Cys Lys Leu Ile Cys Arg Ala Asn Gly
180                610                615                620
183 Thr Gly Tyr Phe Tyr Val Leu Ala Pro Lys Val Val Asp Gly Thr Leu

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184 625          630          635          640
187 Cys Ser Pro Asp Ser Thr Ser Val Cys Val Gln Gly Lys Cys Ile Lys
188          645          650          655
191 Ala Gly Cys Asp Gly Asn Leu Gly Ser Lys Lys Arg Phe Asp Lys Cys
192          660          665          670
195 Gly Val Cys Gly Gly Asp Asn Lys Ser Cys Lys Lys Val Thr Gly Leu
196          675          680          685
199 Phe Thr Lys Pro Met His Gly Tyr Asn Phe Val Val Ala Ile Pro Ala
200          690          695          700
203 Gly Ala Ser Ser Ile Asp Ile Arg Gln Arg Gly Tyr Lys Gly Leu Ile
204 705          710          715          720
207 Gly Asp Asp Asn Tyr Leu Ala Leu Lys Asn Ser Gln Gly Lys Tyr Leu
208          725          730          735
211 Leu Asn Gly His Phe Val Val Ser Ala Val Glu Arg Asp Leu Val Val
212          740          745          750
215 Lys Gly Ser Leu Leu Arg Tyr Ser Gly Thr Gly Thr Ala Val Glu Ser
216          755          760          765
219 Leu Gln Ala Ser Arg Pro Ile Leu Glu Pro Leu Thr Val Glu Val Leu
220          770          775          780
223 Ser Val Gly Lys Met Thr Pro Pro Arg Val Arg Tyr Ser Phe Tyr Leu
224 785          790          795          800
227 Pro Lys Glu Pro Arg Glu Asp Lys Ser Ser His Pro Lys Asp Pro Arg
228          805          810          815
231 Gly Pro Ser Val Leu His Asn Ser Val Leu Ser Leu Ser Asn Gln Val
232          820          825          830
235 Glu Gln Pro Asp Asp Arg Pro Pro Ala Arg Trp Val Ala Gly Ser Trp
236          835          840          845
239 Gly Pro Cys Ser Ala Ser Cys Gly Ser Gly Leu Gln Lys Arg Ala Val
240          850          855          860
243 Asp Cys Arg Gly Ser Ala Gly Gln Arg Thr Val Pro Ala Cys Asp Ala
244 865          870          875          880
247 Ala His Arg Pro Val Glu Thr Gln Ala Cys Gly Glu Pro Cys Pro Thr
248          885          890          895
251 Trp Glu Leu Ser Ala Trp Ser Pro Cys Ser Lys Ser Cys Gly Arg Gly
252          900          905          910
255 Phe Gln Arg Arg Ser Leu Lys Cys Val Gly His Gly Gly Arg Leu Leu
256          915          920          925
259 Ala Arg Asp Gln Cys Asn Leu His Arg Lys Pro Gln Glu Leu Asp Phe
260          930          935          940
263 Cys Val Leu Arg Pro Cys
264 945          950
267 <210> SEQ ID NO: 2
268 <211> LENGTH: 2853
269 <212> TYPE: DNA
270 <213> ORGANISM: Homo sapiens
272 <400> SEQUENCE: 2
273 atgcttttgc tgggcatcct aaccctggct ttcgccgggc gaaccgctgg aggcttttgag      60
275 ccagagcggg aggtagtcgt tcccatccga ctggaccggg acattaacgg ccgccgctac      120
277 tactggcggg gtcccagga ctccgggat cagggaactca ttttcagat cacagcattt      180

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279 caggaggact tttacctaca cctgacgcgc gatgctcagt tottggtccc cgccttctcc 240
281 actgagcacc tgggcgtccc cctccagggg ctcaccgggg gctcttcaga cctgcgacgc 300
283 tgcttctatt ctggggacgt gaacgccgag ccggactcgt tcgctgctgt gagcctgtgc 360
285 ggggggctcc gcggagcctt tggctaccga ggccgcgagt atgtcattag cccgctgccc 420
287 aatgctagcg cgcggcgggc gcagcgcaac agccaggggc cacaccttct ccagcgccgg 480
289 ggtgttccgg gcgggccttc cggagacccc acctctcgct gcgggggtggc ctcgggctgg 540
291 aaccccgcca tcctacgggc cctggaccct tacaagccgc ggccggcggg cttcggggag 600
293 agtcgtagcc ggccgaggtc tgggcgcgcc aagcgtttcg tgtctatccc gcggtacgtg 660
295 gagacgctgg tggtcgcgga cgagtcagt gtcaggttcc acggcgcgga cctggaacat 720
297 tatctgctga cgtcgtctgg aacggcgggc cgactctacc gccatccag catcctcaac 780
299 cccatcaaca tcgttgtgt caaggtgtgt cttcttagag atcgtgactc cgggcccag 840
301 gtcaccgcca atgcggccct gacgtgcgc aacttctgtg cctggcagaa gaagctaac 900
303 aaagtgtgtg acaagcacc cgagtactgg gacactgcca tcctcttcac caggcaggac 960
305 ctgtgtggag ccaccacctg tgacacctg ggcatggctg atgtgggtac catgtgtgac 1020
307 cccaagagaa gctgctctgt cattgaggac gatgggcttc catcagcctt caccactgcc 1080
309 cagagctgg gccagctgtt caacatgccc catgacaatg tgaagtctg tgaggaggtg 1140
311 tttgggaagc tccgagccaa ccacatgatg tccccgacce tcacccagat cgaccgtgcc 1200
313 aaccctggt cagcctgcag tgcctccatc atcaccgact tcctggacag cgggcacggt 1260
315 gactgcctcc tggaccaacc cagcaagccc atctccctgc ccgaggatct gccggcgcc 1320
317 agctacaccc tgagccagca gtgcgagctg gcttttggcg tgggctccaa gccctgtcct 1380
319 tacatgcagt actgcaccaa gctgtgtgtc accgggaagg ccaagggaca gatggtgtgc 1440
321 cagaccgcc acttccctg ggccgatggc accagctgtg gcgagggcaa gctctgcctc 1500
323 aaagggcct gcgtggagag acacaacctc aacaagcaca ggggtgatgg ttcctgggcc 1560
325 aaatgggac cctatggccc ctgctcgcgc acatgtgggt ggggcgtgca gctggccagg 1620
327 aggcagtga ccaacccac ccctgccaac gggggcaagt actgcgaggg agtgagggtg 1680
329 aaataccgat cctgcaacct ggagccctgc ccagctcag cctccggaaa gagcttccgg 1740
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333 gtggcatggg tgcccaagta ctccggctg tctcccggg acaagtgcaa gctcatctgc 1860
335 cgagccaatg gcactggcta cttctatgtg ctggcaccga agtggtgga cggcacgctg 1920
337 tgcctcctg actccacctc cgtctgtgtc caaggcaagt gcatcaaggc tggctgtgat 1980
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359 aagcggggcg tggactgcc gggctccgcc gggcagcgca cggctccctg ctgtgatgca 2640
361 gcccatcgcc ccgtggagac acaagcctgc ggggagccct gcccacctg ggagctcagc 2700
363 gcctgtcac cctgctcaa gagctgcggc cggggatttc agaggcgctc actcaagtgt 2760
365 gtgggccaag gagccggct gctggcccg gaccagtga acttgcaacc caagccccag 2820
367 gagctggact tctgctcct gaggcctgc tga 2853
370 <210> SEQ ID NO: 3
371 <211> LENGTH: 50
372 <212> TYPE: DNA
373 <213> ORGANISM: Homo sapiens

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375 <400> SEQUENCE: 3
376 ctagcgcggc cgcaggatcc gactacaagg acgacgatga caaatgataa 50
379 <210> SEQ ID NO: 4
380 <211> LENGTH: 50
381 <212> TYPE: DNA
382 <213> ORGANISM: Homo sapiens
384 <400> SEQUENCE: 4
385 gatcttatca tttgtcatcg tcgtccttgt agtcggatcc tgcggccgcg 50
388 <210> SEQ ID NO: 5
389 <211> LENGTH: 34
390 <212> TYPE: DNA
391 <213> ORGANISM: Homo sapiens
393 <400> SEQUENCE: 5
394 ggactagtct agaagctggg taccagctgc tagc 34
397 <210> SEQ ID NO: 6
398 <211> LENGTH: 29
399 <212> TYPE: DNA
400 <213> ORGANISM: Homo sapiens
402 <400> SEQUENCE: 6
403 ggactagtgt cgaccgggtca tggctgcgc 29
406 <210> SEQ ID NO: 7
407 <211> LENGTH: 42
408 <212> TYPE: DNA
409 <213> ORGANISM: Homo sapiens
411 <400> SEQUENCE: 7
412 gtgtctagag ccattgctttt gctgggcatc ctaaccctgg ct 42
415 <210> SEQ ID NO: 8
416 <211> LENGTH: 41
417 <212> TYPE: DNA
418 <213> ORGANISM: Homo sapiens
420 <400> SEQUENCE: 8
421 agagcgggccg cctgtcctc ccggaagctc ttccggagg c 41
424 <210> SEQ ID NO: 9
425 <211> LENGTH: 27
426 <212> TYPE: DNA
427 <213> ORGANISM: Homo sapiens
429 <400> SEQUENCE: 9
430 aagcacaggg tggatggttc ctgggcc 27
433 <210> SEQ ID NO: 10
434 <211> LENGTH: 37
435 <212> TYPE: DNA
436 <213> ORGANISM: Homo sapiens
438 <400> SEQUENCE: 10
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442 <210> SEQ ID NO: 11
443 <211> LENGTH: 37
444 <212> TYPE: DNA
445 <213> ORGANISM: Homo sapiens
447 <400> SEQUENCE: 11

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/009,332

DATE: 01/14/2002

TIME: 12:00:36

Input Set : A:\Q67541 Sequence Listing.txt

Output Set: N:\CRF3\01142002\J009332.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date